



SEQUENCE LISTING

#6

<110> Andersson, Leif
Luthman, L. Holger
Marklund, Stefan

<120> VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT

<130> 11145-007001

<140> US 09/826,581
<141> 2001-04-05

<150> US 60/195,665
<151> 2000-04-07

<160> 14

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 821
<212> DNA
<213> Homo sapiens

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ttctcgtgaa	tatggcatg	tgcatttttgc	ggcatatgt	tttgtgatgt	gtgtggttct	540
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ccacagaccc	tttcctggag	cagccttggg	ggttctgagc	atcaaggtag	ggagaatgcc	780
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<211> 989
<212> DNA
<213> Homo sapiens

<400> 2

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tgagatggac	aaggcagaag	tccgtggagg	aaggggagcc	accaggtcag	gggaagggtg	180
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gggtctggtc	tctacctcag	gtccctccat	aacacagagt	tggacccaaac	cttcatcttg	300
tggcctcagt	ctccctacat	agttagagaac	aaggcactgc	agtgccagag	gccagcatgg	360

ccaactcaga aagatggac agagccacta cctgggcga ctctcaggc	420
ctgcaaata ggcacagca tccaggctt ccactgctc tgtgagatga atggcgacag	480
cagatgaga cgtgtttgg aagatggagt tactgtcctc ttcccctcct cccccaaaca	540
ggtccccgtt ccaggccagc tgctgagtc accgggctgg aggccacatt ccccaagacc	600
acacccttg ctcaagctga tcctgccgg gtggcactc caccaacagg gtgggactgc	660
ctccccctcg actgtacagc ctcagctgca ggctccagca cagatgatgt ggagctggcc	720
acggagttcc cagccacaga ggcctggag tgtgagctag aaggcctgct ggaagagagg	780
cctccctgt gcctgtcccc gcaggccccca ttcccaagc tgggctggga tgacgaactg	840
cggaaacccg gcgcccagat ctacatgcgc ttcatgcagg agcacacctg ctacgatgcc	900
atggcaacta gctccaagct agtcatctt gacaccatgc tggaggtgag gccacggctc	960
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<210> 3

<211> 1722

<212> DNA

<213> Homo sapiens

<400> 3

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ggagatggag gaggtgaggg ggagatctt tacgggttgtt ctggggctga tctctgatat	180
accacaagct tggcttcagg ccaagcccaag ccaggggcca gggtgagga aagtccatcc	240
ggagtctgca tggccagctg ggagaccctg gggctcaatt tccccatctg tggagccgct	300
atgaccagct gacacccctt acctccgcta ctgcatggcc ctgtgccata ggtgctaggg	360
agcaaatggg gggaggcagg agagaaagag ccccaactt caggcctggg gggctgcccc	420
actgtcctgt tcccacagtc cccactgtgt ctcagcacaa ggacactggc aggtgtggga	480
ggggatctga ccctcaacctt gccttccacc caaaggcccc gggctgaccc cttccccc	540
cctccctgc agggatgctg accatcactg acttcatctt ggtgctgcat cgctactaca	600
gttccccctt ggtgaggagt gggctggaa tcttatggc acccagaggg gcgggggcgg	660
aggggagtcc tcctggagcc tgggtccctta gaagcccacg tctttctgac ttctggagtc	720
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tatccaagat ttgggcattcg gcacattccg agacttggct tgggtgttgg agacagcacc	1620
catcctgact gcactggaca tctttgttgg ccggcgtgt tctgcactgc ctgtggtaaa	1680
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<210> 4

<211> 1014

<212> DNA

<213> Homo sapiens

<400> 4

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gggtgtggg	atgggtggg	ggcctctgt	gaccagggg	accttgacaa	gtatgcaggg	180
gttgacatct	gtagggtagg	agcccagca	agggggtgac	taggagccat	acttctct	240
ctgccccagc	acctggctgc	ccagcaaacc	tacaaccacc	tggacatgag	tgtggagaa	300
gccctgaggc	agaggacact	atgtctggag	ggagtccctt	cctgccagcc	ccacgagagc	360
ttgggggaag	tgatcgacag	attgctcg	gacgaggtac	cgtgtccct	ccattcatgc	420
ccccaaacaca	tatagcccag	tccttctcat	gcacggctcc	agccatccct	gaacatcggg	480
cacctggcct	atccttccat	ttcatgacca	actcctggt	cccacactgg	cctgcacctg	540
gtcctgtcca	tggggccctt	atgccagggg	tcactgccaa	ctgatcacct	taggcccgtc	600
acaccatccc	taactggttt	ctaggagacg	ctctctccct	cagtcatgtt	gggttgttcc	660
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gaacattgcg	gaccacagg	tacacaggt	ggtgctagtg	gacgagaccc	agcatctctt	780
ggcgctggc	tccctctccg	acatccttca	ggcactggt	ctcagccctg	ctggcatcga	840
tgcctcggg	gcctgagaag	atctgatcc	tcaatccaa	gccacctgca	cacctggaag	900
ccaatgaagg	gaactggaga	actcagcctt	catctcccc	caccccccatt	tgctggttca	960
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<210> 5

<211> 1647

<212> DNA

<213> Homo sapiens

<220>

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<222> (20)...(1486)

<400> 5

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		1				5				10			

acc	cct	tcc	tgg	agc	agc	ctt	ggg	ggt	tct	gag	cat	caa	gag	atg	agc	100
Thr	Pro	Ser	Trp	Ser	Ser	Leu	Gly	Gly	Ser	Glu	His	Gln	Glu	Met	Ser	
						15			20			25				

tcc	cta	gag	caa	gaa	aac	agc	agc	tca	tgg	cca	tca	cca	gct	gtg	acc	148
Phe	Leu	Glu	Gln	Glu	Asn	Ser	Ser	Ser	Trp	Pro	Ser	Pro	Ala	Val	Thr	
						30			35			40				

agc	agc	tca	gaa	aga	atc	cgt	ggg	aaa	cg	agg	gcc	aaa	gcc	ttg	aga	196
Ser	Ser	Ser	Glu	Arg	Ile	Arg	Gly	Lys	Arg	Arg	Ala	Lys	Ala	Leu	Arg	
						45			50			55				

tgg	aca	agg	cag	aag	tcg	gtg	gag	gaa	ggg	gag	cca	cca	ggt	cag	ggg	244
Trp	Thr	Arg	Gln	Lys	Ser	Val	Glu	Gly	Glu	Pro	Pro	Gly	Gln	Gly		
						60			65			70		75		

gaa	ggt	ccc	cgg	tcc	agg	cca	gct	gct	gag	tcc	acc	ggg	ctg	gag	gcc	292
Glu	Gly	Pro	Arg	Ser	Arg	Pro	Ala	Ala	Glu	Ser	Thr	Gly	Leu	Glu	Ala	
						80			85			90				

aca ttc ccc aag acc aca ccc ttg gct caa gct gat cct gcc ggg gtg Thr Phe Pro Lys Thr Thr Pro Leu Ala Gln Ala Asp Pro Ala Gly Val 95 100 105	340
ggc act cca cca aca ggg tgg gac tgc ctc ccc tct gac tgt aca gcc Gly Thr Pro Pro Thr Gly Trp Asp Cys Leu Pro Ser Asp Cys Thr Ala 110 115 120	388
tca gct gca ggc tcc agc aca gat gat gtg gag ctg gcc acg gag ttc Ser Ala Ala Gly Ser Ser Thr Asp Asp Val Glu Leu Ala Thr Glu Phe 125 130 135	436
cca gcc aca gag gcc tgg gag tgt gag cta gaa ggc ctg ctg gaa gag Pro Ala Thr Glu Ala Trp Glu Cys Glu Leu Glu Gly Leu Leu Glu Glu 140 145 150 155	484
agg cct gcc ctg tgc ctg tcc ccg cag gcc cca ttt ccc aag ctg ggc Arg Pro Ala Leu Cys Leu Ser Pro Gln Ala Pro Phe Pro Lys Leu Gly 160 165 170	532
tgg gat gac gaa ctg cgg aaa ccc ggc gcc cag atc tac atg cgc ttc Trp Asp Asp Glu Leu Arg Lys Pro Gly Ala Gln Ile Tyr Met Arg Phe 175 180 185	580
atg cag gag cac acc tgc tac gat gcc atg gca act agc tcc aag cta Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser Lys Leu 190 195 200	628
gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt gct ctg Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe Ala Leu 205 210 215	676
gtg gcc aac ggt gtg cgg gca gcc cct cta tgg gac agc aag aag cag Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys Lys Gln 220 225 230 235	724
agc ttt gtg ggg atg ctg acc atc act gac ttc atc ctg gtg ctg cat Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val Leu His 240 245 250	772
cgc tac tac agg tcc ccc ctg gtc cag atc tat gag att gaa caa cat Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu Gln His 255 260 265	820
aag att gag acc tgg agg gag atc tac ctg caa ggc tgc ttc aag cct Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe Lys Pro 270 275 280	868
ctg gtc tcc atc tct cct aat gat agc ctg ttt gaa gct gtc tac acc Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val Tyr Thr 285 290 295	916
ctc atc aag aac cgg atc cat cgc ctg cct gtt ctt gac ccg gtg tca	964

Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro Val Ser			
300	305	310	315
ggc aac gta ctc cac atc ctc aca cac aaa cgc ctg ctc aag ttc ctg			1012
Gly Asn Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys Phe Leu			
320	325	330	
cac atc ttt ggt tcc ctg ctg ccc cg ^g ccc tcc ttc ctc tac cgc act			1060
His Ile Phe Gly Ser Leu Leu Pro Arg Pro Ser Phe Leu Tyr Arg Thr			
335	340	345	
atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gct gtg gtg ctg			1108
Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val Val Leu			
350	355	360	
gag aca gca ccc atc ctg act gca ctg gac atc ttt gtg gac cgg cgt			1156
Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp Arg Arg			
365	370	375	
gtg tct gca ctg cct gtg gtc aac gaa tgt ggt cag gtc gtg ggc ctc			1204
Val Ser Ala Leu Pro Val Val Asn Glu Cys Gly Gln Val Val Gly Leu			
380	385	390	395
tat tcc cgc ttt gat gtg att cac ctg gct gcc cag caa acc tac aac			1252
Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr Tyr Asn			
400	405	410	
cac ctg gac atg agt gtg gga gaa gcc ctg agg cag agg aca cta tgt			1300
His Leu Asp Met Ser Val Gly Glu Ala Leu Arg Gln Arg Thr Leu Cys			
415	420	425	
ctg gag gga gtc ctt tcc tgc cag ccc cac gag agc ttg ggg gaa gtg			1348
Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Ser Leu Gly Glu Val			
430	435	440	
atc gac agg att gct cgg gag cag gta cac agg ctg gtg cta gtg gac			1396
Ile Asp Arg Ile Ala Arg Glu Gln Val His Arg Leu Val Leu Val Asp			
445	450	455	
gag acc cag cat ctc ttg ggc gtg gtc tcc ctc tcc gac atc ctt cag			1444
Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile Leu Gln			
460	465	470	475
gca ctg gtg ctc agc cct gct ggc atc gat gcc ctc ggg gcc			1486
Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala			
480	485		
tgagaagatc tgagtccatca atccccaggcc acctgcacac ctggaaagcca atgaaggaa			1546
ctggagaact cagccattcat cttccccac ccccatggc tggttcagct atgattcagg			1606
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<212> PRT

<213> Homo sapiens

<400> 6

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 20 25 30
 Asn Ser Ser Ser Trp Pro Ser Pro Ala Val Thr Ser Ser Ser Glu Arg
 35 40 45
 Ile Arg Gly Lys Arg Arg Ala Lys Ala Leu Arg Trp Thr Arg Gln Lys
 50 55 60
 Ser Val Glu Glu Gly Glu Pro Pro Gly Gln Gly Glu Gly Pro Arg Ser
 65 70 75 80
 Arg Pro Ala Ala Glu Ser Thr Gly Leu Glu Ala Thr Phe Pro Lys Thr
 85 90 95
 Thr Pro Leu Ala Gln Ala Asp Pro Ala Gly Val Gly Thr Pro Pro Thr
 100 105 110
 Gly Trp Asp Cys Leu Pro Ser Asp Cys Thr Ala Ser Ala Ala Gly Ser
 115 120 125
 Ser Thr Asp Asp Val Glu Leu Ala Thr Glu Phe Pro Ala Thr Glu Ala
 130 135 140
 Trp Glu Cys Glu Leu Glu Gly Leu Leu Glu Glu Arg Pro Ala Leu Cys
 145 150 155 160
 Leu Ser Pro Gln Ala Pro Phe Pro Lys Leu Gly Trp Asp Asp Glu Leu
 165 170 175
 Arg Lys Pro Gly Ala Gln Ile Tyr Met Arg Phe Met Gln Glu His Thr
 180 185 190
 Cys Tyr Asp Ala Met Ala Thr Ser Ser Lys Leu Val Ile Phe Asp Thr
 195 200 205
 Met Leu Glu Ile Lys Lys Ala Phe Phe Ala Leu Val Ala Asn Gly Val
 210 215 220
 Arg Ala Ala Pro Leu Trp Asp Ser Lys Lys Gln Ser Phe Val Gly Met
 225 230 235 240
 Leu Thr Ile Thr Asp Phe Ile Leu Val Leu His Arg Tyr Tyr Arg Ser
 245 250 255
 Pro Leu Val Gln Ile Tyr Glu Ile Glu Gln His Lys Ile Glu Thr Trp
 260 265 270
 Arg Glu Ile Tyr Leu Gln Gly Cys Phe Lys Pro Leu Val Ser Ile Ser
 275 280 285
 Pro Asn Asp Ser Leu Phe Glu Ala Val Tyr Thr Leu Ile Lys Asn Arg
 290 295 300
 Ile His Arg Leu Pro Val Leu Asp Pro Val Ser Gly Asn Val Leu His
 305 310 315 320
 Ile Leu Thr His Lys Arg Leu Leu Lys Phe Leu His Ile Phe Gly Ser
 325 330 335

 Leu Leu Pro Arg Pro Ser Phe Leu Tyr Arg Thr Ile Gln Asp Leu Gly
 340 345 350
 Ile Gly Thr Phe Arg Asp Leu Ala Val Val Leu Glu Thr Ala Pro Ile
 355 360 365
 Leu Thr Ala Leu Asp Ile Phe Val Asp Arg Arg Val Ser Ala Leu Pro
 370 375 380
 Val Val Asn Glu Cys Gly Gln Val Val Gly Leu Tyr Ser Arg Phe Asp

385	390	395	400
Val Ile His Leu Ala Ala Gln Gln	Thr Tyr Asn His Leu Asp Met Ser		
405	410	415	
Val Gly Glu Ala Leu Arg Gln Arg	Thr Leu Cys Leu Glu Gly Val Leu		
420	425	430	
Ser Cys Gln Pro His Glu Ser Leu Gly Glu Val Ile Asp Arg Ile Ala			
435	440	445	
Arg Glu Gln Val His Arg Leu Val Leu Val Asp Glu Thr Gln His Leu			
450	455	460	
Leu Gly Val Val Ser Leu Ser Asp Ile Leu Gln Ala Leu Val Leu Ser			
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<210> 7
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated primer

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24

<210> 8
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated primer

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25

<210> 9
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated primer

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24

<210> 10
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated primer

<400> 10
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<210> 11
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated primer

<400> 11
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<210> 12
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated primer

<400> 12
acagggatgg catgagaaac cctgc 25

<210> 13
<211> 25
<212> DNA
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<220>
<223> Synthetically generated primer

<400> 13
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<210> 14
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated primer

<400> 14
gacctgtgag tccttacact tgcag 25